

BLAST! 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query: seq6  
(252 letters)

Database: blastrge.txt  
7 sequences; 13,979 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gb AF016295.1 AF016295 Homo sapiens Ets transcription factor (EL...	500	e-144
gb AR020776.1 AR020776 Sequence 1 from patent US 5789200	500	e-144
gb U97156.1 HSU97156 Homo sapiens epithelial-specific ets protei...	500	e-144
gb U73843.1 HSU73843 Homo sapiens epithelial-specific transcript...	500	e-144
gb AF017307.1 AF017307 Homo sapiens Ets-related transcription fa...	500	e-144
gb U66894.1 HSU66894 Human epithelium-restricted Ets protein ESX...	500	e-144
gb U73844.1 HSU73844 Homo sapiens epithelial-specific transcript...	412	e-118

>gb|AF016295.1|AF016295 Homo sapiens Ets transcription factor (ELF3) mRNA,  
complete cds  
Length = 1920

Score = 500 bits (252), Expect = e-144  
Identities = 252/252 (100%)  
Strand = Plus / Plus

```
Query: 1  aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 60
          |||
Sbjct: 424 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 483

Query: 61  cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120
          |||
Sbjct: 484 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 543

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 180
          |||
Sbjct: 544 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 603

Query: 181 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240
          |||
Sbjct: 604 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 663

Query: 241 tgtggcgagga 252
```

|||||  
Sbjct: 664 tgtggcgagga 675

>gb|AR020776.1|AR020776 Sequence 1 from patent US 5789200  
Length = 1920

Score = 500 bits (252), Expect = e-144  
Identities = 252/252 (100%)  
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 60  
|||||  
Sbjct: 424 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 483

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120  
|||||  
Sbjct: 484 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 543

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 180  
|||||  
Sbjct: 544 gagaaggatggcatggccttccaggaggccctagaccaggccctttgaccagggcagc 603

Query: 181 ccctttgccagagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240  
|||||  
Sbjct: 604 ccctttgccagagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 663

Query: 241 tgtggcgagga 252  
|||||  
Sbjct: 664 tgtggcgagga 675

>gb|U97156.1|HSU97156 Homo sapiens epithelial-specific ets protein (jen) mRNA,  
complete  
cds  
Length = 1942

Score = 500 bits (252), Expect = e-144  
Identities = 252/252 (100%)  
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 60  
|||||  
Sbjct: 434 aattgtgcccttgaggagctgcgtctgggtctttgggcctctgggggaccaactccatgcc 493

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120  
|||||  
Sbjct: 494 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 553

Query: 121 gagaaggatggcatggccttccaggaggccctagacccagggccctttgaccagggcagc 180  
|||||  
Sbjct: 554 gagaaggatggcatggccttccaggaggccctagacccagggccctttgaccagggcagc 613

Query: 181 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240  
|||||  
Sbjct: 614 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 673

Query: 241 tgtggcgagga 252  
|||||  
Sbjct: 674 tgtggcgagga 685

Score = 22.3 bits (11), Expect = 0.65  
Identities = 11/11 (100%)  
Strand = Plus / Plus

Query: 231 ccccgagcagct 241  
|||||  
Sbjct: 694 ccccgagcagct 704

Score = 22.3 bits (11), Expect = 0.65  
Identities = 11/11 (100%)  
Strand = Plus / Plus

Query: 144 ggaggccctag 154  
|||||  
Sbjct: 1587 ggaggccctag 1597

>gb|U73843.1|HSU73843 Homo sapiens epithelial-specific transcription factor ESE-1b  
(ESE-1) mRNA, complete cds  
Length = 1915

Score = 500 bits (252), Expect = e-144  
Identities = 252/252 (100%)  
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 60  
|||||  
Sbjct: 429 aattgtgcccttgaggagctgcgtctggtctttgggcctctgggggaccaactccatgcc 488

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120  
|||||  
Sbjct: 489 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 548

Query: 121 gagaaggatggcatggccttccaggaggccctagacccagggccctttgaccagggcagc 180  
|||||

Sbjct: 549 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 608

Query: 181 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240

|||||

Sbjct: 609 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 668

Query: 241 tgtggcgagga 252

|||||

Sbjct: 669 tgtggcgagga 680

Score = 22.3 bits (11), Expect = 0.65

Identities = 11/11 (100%)

Strand = Plus / Plus

Query: 144 ggaggccctag 154

|||||

Sbjct: 1583 ggaggccctag 1593

>gb|AF017307.1|AF017307 Homo sapiens Ets-related transcription factor (ERT)  
mRNA, complete

cds

Length = 2529

Score = 500 bits (252), Expect = e-144

Identities = 252/252 (100%)

Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgctctggtctttgggcctctgggggaccaactccatgcc 60

|||||

Sbjct: 512 aattgtgcccttgaggagctgcgctctggtctttgggcctctgggggaccaactccatgcc 571

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120

|||||

Sbjct: 572 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 631

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 180

|||||

Sbjct: 632 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 691

Query: 181 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240

|||||

Sbjct: 692 ccctttgccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 751

Query: 241 tgtggcgagga 252

|||||

Sbjct: 752 tgtggcgagga 763

Score = 22.3 bits (11), Expect = 0.65  
Identities = 11/11 (100%)  
Strand = Plus / Plus

Query: 231 ccccggcagct 241  
          |||||  
Sbjct: 772 ccccggcagct 782

Score = 22.3 bits (11), Expect = 0.65  
Identities = 11/11 (100%)  
Strand = Plus / Plus

Query: 144 ggaggccctag 154  
          |||||  
Sbjct: 1665 ggaggccctag 1675

>gb|U66894.1|HSU66894 Human epithelium-restricted Ets protein ESX mRNA, complete  
cds

Length = 1907

Score = 500 bits (252), Expect = e-144  
Identities = 252/252 (100%)  
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgcgtctggtccttgggcctctgggggaccaactccatgcc 60  
          |||||  
Sbjct: 405 aattgtgcccttgaggagctgcgtctggtccttgggcctctgggggaccaactccatgcc 464

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120  
          |||||  
Sbjct: 465 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 524

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggggcctttgaccagggcagc 180  
          |||||  
Sbjct: 525 gagaaggatggcatggccttccaggaggccctagaccaggggcctttgaccagggcagc 584

Query: 181 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 240  
          |||||  
Sbjct: 585 ccctttgcccaggagctgctggacgacggtcagcaagccagcccctaccaccccggcagc 644

Query: 241 tgtggcgagga 252  
          |||||  
Sbjct: 645 tgtggcgagga 656

Score = 22.3 bits (11), Expect = 0.65  
Identities = 11/11 (100%)

Strand = Plus / Plus

Query: 144 ggaggccctag 154  
          |||||  
Sbjct: 1559 ggaggccctag 1569

>gb|U73844.1|HSU73844 Homo sapiens epithelial-specific transcription factor ESE-  
1a  
          (ESE-1) mRNA, complete cds  
          Length = 1846

Score = 412 bits (208), Expect = e-118  
Identities = 208/208 (100%)  
Strand = Plus / Plus

Query: 1 aattgtgcccttgaggagctgCGTctgtgtttgggcctctgggggaccaactccatgcc 60  
          |||||  
Sbjct: 429 aattgtgcccttgaggagctgCGTctgtgtttgggcctctgggggaccaactccatgcc 488

Query: 61 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 120  
          |||||  
Sbjct: 489 cagctgcgagacctcacttccagctcttctgatgagctcagttggatcattgagctgctg 548

Query: 121 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 180  
          |||||  
Sbjct: 549 gagaaggatggcatggccttccaggaggccctagaccaggggccctttgaccagggcagc 608

Query: 181 ccctttgccaggagctgctggacgacg 208  
          |||||  
Sbjct: 609 ccctttgccaggagctgctggacgacg 636

Score = 22.3 bits (11), Expect = 0.65  
Identities = 11/11 (100%)  
Strand = Plus / Plus

Query: 144 ggaggccctag 154  
          |||||  
Sbjct: 1514 ggaggccctag 1524

Database: blastrge.txt  
Posted date: Nov 30, 1999 9:59 AM  
Number of letters in database: 13,979  
Number of sequences in database: 7

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda      K      H  
1.37      0.711      1.31

Matrix: blastn matrix:1 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 28  
Number of Sequences: 7  
Number of extensions: 28  
Number of successful extensions: 28  
Number of sequences better than 10.0: 7  
length of query: 252  
length of database: 13,979  
effective HSP length: 11  
effective length of query: 241  
effective length of database: 13,902  
effective search space: 3350382  
effective search space used: 3350382  
T: 0  
A: 0  
X1: 6 (11.9 bits)  
X2: 25 (49.6 bits)  
S1: 12 (24.3 bits)  
S2: 10 (20.3 bits)